**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in this application.

Listing of Claims:

Claims 1-11 (cancelled)

12. (Withdrawn) A method for evaluating the potential of a chemical entity to associate with:

a) a molecule or molecular complex comprising a binding pocket defined by structure coordinates of JNK3 amino acids Ile70, Gly71, Ser72, Gly73, Ala74, Gln75, Gly76, Val78, Ala91, Lys93, Glu111, Ile124, Met146, Glu147, Leu148, Met149, Asp150, Ala151, Asn152, Gln155, Lys191, Ser193, Asn194, Val196 and Leu206 according to Figure 1; or

b) a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å,

said method comprising the steps of:

(i) employing computational means to perform a fitting operation between the chemical entity and a binding pocket of the molecule or molecular complex; and

(ii) analyzing the results of said fitting operation to quantify the association between the chemical entity and the binding pocket; and

(iii) outputting said quantified association to a suitable output hardware.

13. (Withdrawn) The method according to claim 12, wherein said method evaluates the potential of chemical entity to associate with:

a) a molecular or molecular complex comprising a binding pocket defined by the structural coordinates of JNK3 amino acids Ile70, Gly71, Ser72, Gly73, Ala74, Gln75, Gly76, Ile77, Val78, Cys79, Ala80, Val90, Ala91, Ile92, Lys93, Lys94, Leu95, His104, Arg107, Glu111, Ile124, Ser125, Leu144, Val145, Met146, Glu147, Leu148, Met149, Asp150, Ala151, Asn152, Leu153, Cys154, Gln155, Asp189, Lys191, Pro192, Ser193, Asn194, Ile195, Val196 Val197, Lys204, Leu206 and Asp207, according to Figure 1; or

b) a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.

14. (Withdrawn) The method according to claims 12 or 13, wherein said method evaluates the potential of a chemical entity to associate with a molecule or molecular complex:

a) defined by the set of structure coordinates for JNK3 amino acids, as set forth in Figure 1; or

b) a homologue of said molecule or molecular complex having a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.

Claim 15 (cancelled)

16. (Withdrawn) A method for designing an inhibitor of an unphosphorylated JNK3α (c-Jun N-terminal kinase 3α) molecule, comprising the step of:

using the atomic coordinates in Figure 1A, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å, which describe an active site binding pocket of the unphosphorylated JNK3α, to design or select said inhibitor, where said active site binding pocket comprises the amino acids Ile70, Gly71, Ser72, Gly73, Ala74, Gln75, Gly76, Val78, Ala91, Lys93, Glu111, Ile124, Met146, Glu147, Leu148, Met149, Asp150, Ala151, Asn152, Gln155, Lys191, Ser193, Asn194, Val196 and Leu206.

17. (Withdrawn) The method according to claim 16, wherein said active site binding pocket additionally comprises the amino acids Ile77, Cys79, Ala80, Val90, Ile92, Lys94, Leu95, His104, Arg107, Ser125, Leu144, Val145, Leu153, Cys154, Asp189, Pro192, Ile195, Val197, Lys204 and Asp207.

Claim 18 (cancelled)

19. (Withdrawn) The method according to claims 16 or 17, wherein a potential inhibitor is contacted with said unphosphorylated JNK3α molecule to determine the ability of said potential inhibitor to associate with the unphosphorylated JNK3α molecule.

20. (Withdrawn) A method for designing an inhibitor of an unphosphorylated JNK3α (c-Jun N-terminal kinase 3α) molecule comprising the steps of:

a) producing a crystal of an unphosphorylated JNK3α (c-Jun N-terminal kinase 3α) molecule and a chemical entity, wherein said unphosphorylated JNK3α molecule contains an N-terminal deletion of 39 amino acids;

b) determining the three-dimensional atomic coordinates of amino acids Ile70, Gly71, Ser72, Gly73, Ala74,

Gln75, Gly76, Ile77, Val78, Cys79, Ala80, Val90, Ala91, Ile92, Lys93, Lys94, Leu95, His104, Arg107, Glu111, Ile124, Ser125, Leu144, Val145, Met146, Glu147, Leu148, Met149, Asp150, Ala151, Asn152, Leu153, Cys154, Gln155, Asp189, Lys191, Pro192, Ser193, Asn194, Ile195, Val196 Val197, Lys204, Leu206 and Asp207 of an active site binding pocket of the unphosphorylated JNK3α molecule by X-ray diffraction of the crystal;

c) using said coordinates, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å, to design or select said inhibitor.

21. (Withdrawn) The method according to claim 20, further comprising the step of contacting a potential inhibitor with said unphosphorylated JNK3α molecule to determine the ability of said potential inhibitor to associate with said unphosphorylated JNK3α molecule.

22. (Withdrawn) The method according to claim 20, wherein said unphosphorylated JNK3α molecule further contains a C-terminal deletion of 20 amino acids.

23. (Previously Presented) A method for identifying an inhibitor of an unphosphorylated JNK3α (c-Jun N-terminal kinase 3α) molecule, comprising the step of:

a) using the atomic coordinates of Ile70, Gly71, Ser72, Gly73, Ala74, Gln75, Gly76, Val78, Ala91, Lys93, Glu111, Ile124, Met146, Glu147, Leu148, Met149, Asp150, Ala151, Asn152, Gln155, Lys191, Ser193, Asn194, Val196 and Leu206 according to Figure 1A ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å, to generate a three-dimensional structure of molecule comprising a JNK3α active site binding pocket;

b) employing said three-dimensional structure to design or select a potential inhibitor;

c) synthesizing said potential inhibitor; and

d) contacting said potential inhibitor with said molecule to determine the ability of a potential inhibitor to associate with said molecule.

24. (Previously Presented) The method according to claim 23, wherein the atomic coordinates of Ile70, Gly71, Ser72, Gly73, Ala74, Gln75, Gly76, Ile77, Val78, Cys79, Ala80, Val90, Ala91, Ile92, Lys93, Lys94, Leu95, His104, Arg107, Glu111, Ile124, Ser125, Leu144, Val145, Met146, Glu147,

Leu148, Met149, Asp150, Ala151, Asn152, Leu153, Cys154, Gln155, Asp189, Lys191, Pro192, Ser193, Asn194, Ile195, Val196 Val197, Lys204, Leu206 and Asp207 according to Figure 1A ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å, are used to generate said three-dimensional structure of the molecule comprising a JNK3α active site binding pocket.

25. (Currently Amended) A method for identifying an inhibitor of an unphosphorylated JNK3α (c-Jun N-terminal kinase 3α) molecule, comprising the steps of:

a) producing a crystal of an unphosphorylated JNK3α (c-Jun N-terminal kinase 3α) molecule comprising amino acid residues 40-402 of SEQ ID NO:1 and a chemical entity~~, wherein said unphosphorylated JNK3α molecule contains an N-terminal deletion of 39 amino acids~~;

b) determining the three-dimensional atomic coordinates of amino acids Ile70, Gly71, Ser72, Gly73, Ala74, Gln75, Gly76, Val78, Ala91, Lys93, Glu111, Ile124, Met146, Glu147, Leu148, Met149, Asp150, Ala151, Asn152, Gln155, Lys191, Ser193, Asn194, Val196 and Leu206 of an active site binding pocket of the unphosphorylated JNK3α molecule by X-ray diffraction of the crystal;

c) using the atomic coordinates of Ile70, Gly71, Ser72, Gly73, Ala74, Gln75, Gly76, Val78, Ala91, Lys93, Glu111, Ile124, Met146, Glu147, Leu148, Met149, Asp150, Ala151, Asn152, Gln155, Lys191, Ser193, Asn194, Val196 and Leu206 according to Figure 1A ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å, to generate a three-dimensional structure of molecule comprising a JNK3α active site binding pocket;

d) employing said three-dimensional structure to design or select a potential inhibitor;

e) synthesizing said potential inhibitor; and

f) contacting said potential inhibitor with said molecule to determine the ability of said potential inhibitor to associate with said molecule.

26. (Previously Presented) The method according to claim 25, wherein the atomic coordinates of Ile70, Gly71, Ser72, Gly73, Ala74, Gln75, Gly76, Ile77, Val78, Cys79, Ala80, Val90, Ala91, Ile92, Lys93, Lys94, Leu95, His104, Arg107, Glu111, Ile124, Ser125, Leu144, Val145, Met146, Glu147, Leu148, Met149, Asp150, Ala151, Asn152, Leu153, Cys154, Gln155, Asp189, Lys191, Pro192, Ser193, Asn194, Ile195, Val196 Val197, Lys204, Leu206 and Asp207 according to Figure 1A ± a

root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å, are used to generate said three-dimensional structure of the molecule comprising a JNK3α active site binding pocket.

27. (New) A method for identifying an inhibitor of an unphosphorylated JNK3α (c-Jun N-terminal kinase 3α) molecule, comprising the step of:

a) using the structure coordinates of JNK3α according to Figure 1A ± a root mean square deviation from the backbone atoms of said amino acids of 1.5 Å, to generate a three-dimensional structure of a molecular complex comprising an active site binding pocket of amino acid residues Ile70, Gly71, Ser72, Gly73, Ala74, Gln75, Gly76, Val78, Ala91, Lys93, Glu111, Ile124, Met146, Glu147, Leu148, Met149, Asp150, Ala151, Asn152, Gln155, Lys191, Ser193, Asn194, Val196 and Leu206, wherein said binding site is a binding site for JNK3α;

b) employing said three-dimensional structure to design or select a potential inhibitor;

c) synthesizing said potential inhibitor; and

d) contacting said potential inhibitor with JNK3α to determine the ability of said potential inhibitor to bind to JNK3α.

28. (New) A method for identifying an inhibitor of an unphosphorylated JNK3α (c-Jun N-terminal kinase 3α) molecule:

a) producing a crystal of JNK3α comprising amino acid residues 40-402 of SEQ ID NO:1;

b) determining the three-dimensional structure coordinates of JNK3α using the crystal in step a);

c) using the structure coordinates from step b) to generate a three-dimensional structure of a molecular complex;

d) employing said three-dimensional structure to design or select a potential inhibitor;

e) synthesizing said potential inhibitor; and

f) contacting said potential inhibitor with JNK3α to determine the ability of said potential antagonist to bind to JNK3α.

29. (New) A method for identifying an inhibitor of an unphosphorylated JNK3α (c-Jun N-terminal kinase 3α) molecule:

a) using the structure coordinates of JNK3α according to Figure 1A ± a root mean square deviation from the

backbone atoms of said amino acids of 1.5 Å, to generate a three-dimensional model;

b) identifying an active site binding pocket using the structure coordinates in step a), wherein said active site binding pocket is a binding site for JNK3α, and comprises at least amino acid residues Ile70, Gly71, Ser72, Gly73, Ala74, Gln75, Gly76, Val78, Ala91, Lys93, Glu111, Ile124, Met146, Glu147, Leu148, Met149, Asp150, Ala151, Asn152, Gln155, Lys191, Ser193, Asn194, Val196 and Leu206, and using said residues to generate a three-dimensional binding site;

c) employing said three-dimensional binding site to design or select a potential inhibitor;

d) synthesizing said potential inhibitor; and

e) contacting said potential inhibitor with JNK3α to determine the ability of said potential inhibitor to bind to human JNK3α.